

# SEQUENCE LISTING

<110> Duvick, Jonathan P.  
 Gilliam, Jacob T.  
 Maddox, Joyce R.  
 Rao, Aragula Gururaj  
 Crasta, Oswald R.  
 Folkerts, Otto

<120> Amino Polyol Amine Oxidase  
 Polynucleotides and Related Polypeptides and Methods of Use

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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
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Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
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Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu

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Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	85	90	95	
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag				336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	100	105	110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc				384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	115	120	125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg				432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	130	135	140	
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Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	145	150	155	160
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Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	165	170	175	
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	180	185	190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg				624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	195	200	205	
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Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
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Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser	
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Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln	
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ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac      288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
             85             90             95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag      336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
             100             105             110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc      384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
             115             120             125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg      432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
             130             135             140

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg      480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
             145             150             155             160

cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt      528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
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gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag      576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
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agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg      624
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 <223> Extra lysine in K:trAPAO

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aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	

65	70	75	80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa				288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	85	90	95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag				336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg				384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag				432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	130	135	140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac				480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc				528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc				576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc				624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc				672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc				720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg				768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc				816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa				864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc				912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	290	295	300	

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	1389
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
450 455 460	

tag	1392
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<210> 11  
 <211> 463  
 <212> PRT  
 <213> *Exophiala spinifera*

<400> 11	
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	

65					70					75				80	
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85					90					95	
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
			100						105				110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
	130					135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
				165					170					175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
	195						200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	210					215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
	275						280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
				325					330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
		340						345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
	355						360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385				390						395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
				405					410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
		420						425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
	435					440						445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
	450					455					460				

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into  
expression vectors, N23256

<400> 12  
 ggggaattca aagacaacgt tgcggacgtg gtag 34  
  
 <210> 13  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer sequence designed for cloning DNA into  
 expression vectors, N23259  
  
 <400> 13  
 ggggcggccg cctatgctgc tggcaccagg ctag 34  
  
 <210> 14  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Designed oligonucleotide for 3' RACE, N21965  
  
 <400> 14  
 tggtttcgtt accgacaacc ttgtatccc 29  
  
 <210> 15  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Designed oligonucleotide for 5' race, N21968  
  
 <400> 15  
 gagttggtcc cagacagact tttgtcgt 28  
  
 <210> 16  
 <211> 1673  
 <212> DNA  
 <213> Exophiala spinifera  
  
 <220>  
 <221> sig\_peptide  
 <222> (1)...(267)  
 <223> yeast alpha mating factor secretion signal.  
  
 <221> CDS  
 <222> (1)...(1662)  
  
 <400> 16  
 atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc 48  
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser  
 -85 -80 -75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa	96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln	
-70 -65 -60	
att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc	144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe	
-55 -50 -45	
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg	192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu	
-40 -35 -30	
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta	240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val	
-25 -20 -15 -10	
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg	288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala	
-5 1 5	
gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc	336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg	
10 15 20	
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat	384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp	
25 30 35	
cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg	432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr	
40 45 50 55	
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc	480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser	
60 65 70	
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag	528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln	
75 80 85	
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act	576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr	
90 95 100	
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca	624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala	
105 110 115	
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc	672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser	
120 125 130 135	
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg	720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val	
140 145 150	
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc	768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu	

155	160	165	
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 170 175 180			816
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly 185 190 195			864
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg 200 205 210 215			912
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu 220 225 230			960
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln 235 240 245			1008
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg 250 255 260			1056
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu 265 270 275			1104
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn 280 285 290 295			1152
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro 300 305 310			1200
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp 315 320 325			1248
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp 330 335 340			1296
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln 345 350 355			1344
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala 360 365 370 375			1392
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu 380 385 390			1440



gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc	1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala	
395 400 405	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg	1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr	
410 415 420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg	1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp	
425 430 435	
aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca	1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala	
440 445 450 455	
gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c	1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala	
460 465	

<210> 17  
 <211> 554  
 <212> PRT  
 <213> *Exophiala spinifera*

<220>  
 <221> SIGNAL  
 <222> (1)...(89)

<400> 17																
Met	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser	
				-85					-80					-75		
Ala	Leu	Ala	Ala	Pro	Val	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln	
		-70					-65						-60			
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe	
	-55					-50					-45					
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu	
	-40				-35					-30						
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val	
	-25			-20					-15						-10	
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Glu	Phe	Lys	Asp	Asn	Val	Ala	
		-5							1				5			
Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	
	10						15					20				
Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	
	25					30					35					
Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	
	40			45					50					55		
Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	
		60						65						70		
Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	
		75					80					85				
Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	
	90					95						100				
Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	
	105					110					115					
Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	

120		125		130		135									
Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val
		140							145					150	
Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu
		155						160					165		
Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His
		170					175					180			
Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly
	185					190					195				
Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg
200				205						210				215	
Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu
			220					225					230		
Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln
		235					240						245		
Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg
	250					255					260				
Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu
	265					270					275				
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn
280				285						290				295	
Ser	Ile	Leu	Gly	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	
			300					305					310		
Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp
		315						320					325		
Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp
	330					335					340				
Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln
	345				350					355					
Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala
360				365						370				375	
Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu
			380					385					390		
Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala
		395					400						405		
Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr
	410					415						420			
Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp
	425				430					435					
Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala
440				445						450				455	
Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala						
			460					465							

<210> 18  
 <211> 2079  
 <212> DNA  
 <213> Unknown

<220>  
 <223> GST:K:trAPAO 2079 nt. Translation starting at nt 1  
 - 687, gst fusion + polylinker, 688-2076,  
 K:trAPAO, extra lysine underlined; 2077-2079, stop  
 codon. For bacterial expression.

<221> CDS  
 <222> (1)...(2076)

<221> misc\_feature  
 <222> (1)...(687)  
 <223> gst fusion + polylinker

<221> misc\_feature  
 <222> (688)...(2076)  
 <223> K:trAPAO

<221> misc\_feature  
 <222> (688)...(690)  
 <223> Extra lysine

<400> 18  
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48  
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
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 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
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 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
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 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
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 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
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 165 170 175

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Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
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Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp	
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Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly	
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gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg	2064
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Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp		
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Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe		
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Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr		
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      signal sequence, nucleotides 73-75, added lysine
      residue; nucleotides 76 -1464 , trAPAO cDNA.

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gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg      192
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gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct      384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
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Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala	
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His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala	
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Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser	
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Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly	
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Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu	
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Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys		
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Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser		
265					270					275					280		
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu		
				285				290						295			
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg		
			300				305						310				
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser		
		315				320					325						
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr		
		330				335					340						
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys		
345					350					355					360		
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu		
				365				370						375			
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu		
			380				385					390					
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly		
		395					400					405					
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys		
	410					415					420						
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr		
425					430					435					440		
Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val		
				445				450					455				
Ala	Ser	Leu	Val	Pro	Ala	Ala											
			460														

<210> 22  
 <211> 1803  
 <212> DNA  
 <213> *Exophiala spinifera*

<220>  
 <221> CDS

<222> (1)...(1800)

<400> 22

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1 5 10 15	
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
130 135 140	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145 150 155 160	
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc	576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
180 185 190	
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta	624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val	
195 200 205	
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg	672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
210 215 220	

act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct	720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala	
225 230 235 240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg	768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala	
245 250 255	
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa	816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln	
260 265 270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc	864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe	
275 280 285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta	912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val	
290 295 300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc	960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile	
305 310 315 320	
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt	1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser	
325 330 335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa	1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	
340 345 350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca	1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	
355 360 365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca	1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
370 375 380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa	1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
385 390 395 400	
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt	1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
405 410 415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc	1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
420 425 430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
435 440 445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc	1392

Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile		
450						455					460						
tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	1440	
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile		
465					470					475					480		
acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	1488	
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser		
				485					490					495			
aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	gcc	tac	1536	
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr		
		500						505					510				
gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	1584	
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile		
		515					520					525					
gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	1632	
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr		
	530					535					540						
ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	tcg	gcg	ctc	aga	acg	ccg	ttc	1680	
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe		
545					550					555					560		
aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	aaa	ggg	1728	
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly		
				565					570					575			
tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggg	caa	cga	ggg	gct	gca	gaa	gtt	1776	
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val		
			580					585					590				
gtg	gct	agc	ctg	gtg	cca	gca	gca	tag								1803	
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala										
		595				600											

<210> 23  
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 <212> PRT  
 <213> *Exophiala spinifera*

<400> 23

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro
		35				40						45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
				85					90					95	



Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
565 570 575  
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
580 585 590  
Val Ala Ser Leu Val Pro Ala Ala  
595 600

<210> 24  
<211> 3003  
<212> DNA  
<213> Unknown

<220>  
<223> Sequence is barley alpha amylase signal sequence:  
esp1 mat: an artificial spacer sequence and  
K:trAPAO

<221> sig\_peptide  
<222> (1)...(72)  
<223> Barley alpha amylase signal sequence

<221> misc\_feature  
<222> (73)...(1575)  
<223> esp1 mat

<221> misc\_feature  
<222> (1576)...(1611)  
<223> spacer sequence

<221> misc\_feature  
<222> (1612)...(3000)  
<223> K:trAPAO

<221> CDS  
<222> (1)...(3000)

<221> misc\_feature  
<222> (1612)...(1614)  
<223> Extra lysine

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-20 -15 -10  
ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96  
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala  
-5 1 5  
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc 144  
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr  
10 15 20  
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt 192  
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe  
25 30 35 40



gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act	240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr	
45 50 55	
gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc	288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu	
60 65 70	
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt	336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly	
75 80 85	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag	384
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
90 95 100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa	432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
105 110 115 120	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc	480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	
125 130 135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg	528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	
140 145 150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg	576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	
155 160 165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag ccg aac atc gca	624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
170 175 180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg	672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	
185 190 195 200	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca	720
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro	
205 210 215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc	768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	
220 225 230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc	816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu	
235 240 245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat	864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	
250 255 260	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag	912
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu	

265	270	275	280	
tac acg ttg gac aac gta acg gct gtg	tac cgt tct gaa acg gct cgc			960
Tyr Thr Leu Asp Asn Val Thr Ala Val	Tyr Arg Ser Glu Thr Ala Arg			
285	290	295		
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc				1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala				
300	305	310		
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat				1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr				
315	320	325		
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt				1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu				
330	335	340		
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag				1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln				
345	350	355	360	
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc				1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile				
365	370	375		
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac				1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr				
380	385	390		
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg				1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val				
395	400	405		
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca				1344
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala				
410	415	420		
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc				1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala				
425	430	435	440	
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa				1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln				
445	450	455		
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt				1488
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val				
460	465	470		
gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt				1536
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg				
475	480	485		
tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc				1584
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly				
490	495	500		

agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val 505 510 515 520	1632
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 525 530 535	1680
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 540 545 550	1728
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 555 560 565	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570 575 580	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585 590 595 600	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740 745 750	2304

730	735	740	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 745 750 755 760			2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 765 770 775			2400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 780 785 790			2448
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			2496
795	800	805	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 810 815 820			2544
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 825 830 835 840			2592
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 845 850 855			2640
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 860 865 870			2688
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 875 880 885			2736
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 890 895 900			2784
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 905 910 915 920			2832
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 925 930 935			2880
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 940 945 950			2928
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 955 960 965			2976

gtg gct agc ctg gtg cca gca gca tag  
 Val Ala Ser Leu Val Pro Ala Ala  
 970 975

3003

<210> 25  
 <211> 1000  
 <212> PRT  
 <213> Unknown

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 45 50 55  
 Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu  
 60 65 70  
 Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly  
 75 80 85  
 Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu  
 90 95 100  
 Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu  
 105 110 115 120  
 Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala  
 125 130 135  
 Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu  
 140 145 150  
 Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly  
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 Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala  
 170 175 180  
 Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala  
 185 190 195 200  
 Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro  
 205 210 215  
 Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe  
 220 225 230  
 Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu  
 235 240 245  
 Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp  
 250 255 260  
 Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu  
 265 270 275 280  
 Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg  
 285 290 295  
 Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala  
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Asn	Asp	Gly	Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr
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Leu	Glu	Glu	Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu
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Gly	Ala	Tyr	Pro	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp	Gln
345					350					355					360
Ile	Ala	Ala	Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile
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Val	Ala	Gln	Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr
			380					385					390		
Tyr	Asn	Ala	Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val
		395					400					405			
Tyr	His	Ser	Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala
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Ser	Ala	Thr	Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala
425					430					435					440
Trp	Ala	Ala	Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys	Gln
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Val	Pro	Asn	Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val
			460					465					470		
Asp	Val	Ser	Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg
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Tyr	Tyr	Thr	Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly	Gly
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Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp	Val
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Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
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Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			540					545					550		
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
		555					560					565			
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
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Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
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Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
				605					610					615	
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
			620					625					630		
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln
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Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
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Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val
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Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
				685					690					695	
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser
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Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys
		715					720					725			
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro
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Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala
745					750					755					760
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys
				765					770					775	

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
                     780                    785                    790  
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
                     795                    800                    805  
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
             810                    815                    820  
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
 825                    830                    835                    840  
 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
                     845                    850                    855  
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
                     860                    865                    870  
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
             875                    880                    885  
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
             890                    895                    900  
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
 905                    910                    915                    920  
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
                     925                    930                    935  
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
             940                    945                    950  
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
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 Val Ala Ser Leu Val Pro Ala Ala  
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<211> 2976

<212> DNA

<213> Unknown

<220>

<223> Barley alpha amylase signal sequence: BEST1  
 mature: artificial spacer: and K:trAPAO. For  
 plant expression.

<221> sig\_peptide

<222> (1)...(72)

<223> Barley alpha amylase signal sequence

<221> mat\_peptide

<222> (73)...(1545)

<223> BEST1 mature

<221> misc\_feature

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<222> (1585)...(2973)

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<221> CDS

<222> (1)...(2973)

<221> misc\_feature

<222> (1585)...(1587)

<223> Extra lysine

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Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr	
-5 1 5	
gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc	144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg	
10 15 20	
gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg	192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro	
25 30 35 40	
ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt	240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe	
45 50 55	
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc	288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala	
60 65 70	
ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca	336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	
75 80 85	
ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc	384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	
90 95 100	
ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg	432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	
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ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac	480
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	
125 130 135	
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc	528
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	
140 145 150	
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg	576
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg	
155 160 165	
tgg gtg cag agc aac gcc gcg gcc ttc gga ggg gac ccc ggc cga gtg	624
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	
170 175 180	
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc	672



Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu	
185 190 195 200	
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt	720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser	
205 210 215	
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg	768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser	
220 225 230	
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca	816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro	
235 240 245	
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac	864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp	
250 255 260	
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg	912
Leu Arg Arg Pro Arg Thr Gly Pro Ile Val Asp Gly His Val Leu	
265 270 275 280	
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt	960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val	
285 290 295	
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg	1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly	
300 305 310	
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg	1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala	
315 320 325	
cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac	1104
Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp	
330 335 340	
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat	1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn	
345 350 355 360	
cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag	1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln	
365 370 375	
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga	1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly	
380 385 390	
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg	1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val	
395 400 405	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc	1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro	
410 415 420	

acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc	1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val	
425 430 435 440	
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct	1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro	
445 450 455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc	1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg	
460 465 470	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc	1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly	
475 480 485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc	1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser	
490 495 500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
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ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
525 530 535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
540 545 550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
555 560 565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
570 575 580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
585 590 595 600	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
605 610 615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
620 625 630	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
635 640 645	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	2064

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Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu		
665					670					675					680		
ggt	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	2160	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile		
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aag	agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	2208	
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly		
			700					705						710			
ggg	cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	2256	
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala		
		715					720						725				
atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	2304	
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val		
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gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	2352	
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser		
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ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	2400	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr		
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Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln		
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Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe		
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gta	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	2544	
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu		
	810					815					820						
caa	tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	2592	
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp		
825					830					835					840		
gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	2640	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly		
				845					850					855			
cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	2688	
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp		
			860					865					870				
gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	2736	
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu		
		875					880					885					

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	2784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
890 895 900	

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
905 910 915 920	

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
925 930 935	

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
940 945 950	

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	2973
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955 960 965	

tag	2976
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Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro	
25 30 35 40	
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe	
45 50 55	
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala	
60 65 70	
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	
75 80 85	
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	
90 95 100	
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	
105 110 115 120	
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	
125 130 135	
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	
140 145 150	
Gly Thr Ser Gly Asn Tyr Gly Leu Asp Ile Leu Ala Ala Leu Arg	
155 160 165	
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	

170					175					180				
Thr	Val	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu
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Thr	Ser	Pro	Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu
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Pro	Gly	Leu	Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala
			220					225					230	Ser
Gly	Glu	Arg	Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp
		235					240					245		Pro
Ala	Thr	Leu	Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg
	250					255					260			Asp
Leu	Arg	Arg	Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val
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Pro	Gln	Thr	Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro
			285						290					295
Arg	Val	Leu	Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu
		300						305					310	Gly
Arg	Ala	Pro	Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu
	315						320					325		Ala
Gln	Phe	Gly	Asp	Gln	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp
	330				335				340					
Gly	Arg	Ala	Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp
345				350					355					Asn
Gln	Phe	Asn	Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg
			365					370					375	Gln
Gly	Ala	Pro	Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly
	380						385					390		Gly
Arg	Ala	Pro	Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly
	395					400					405			Val
Phe	Lys	Leu	Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly
	410				415					420				Pro
Thr	Pro	Ala	Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp
425				430					435					440
Arg	Phe	Ala	Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp
			445					450					455	Pro
Ala	Tyr	Ser	Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly
	460						465						470	Arg
Ala	Ala	Val	Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp
	475					480					485			Gly
Ala	Lys	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser
	490				495					500				
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser
505				510					515					Gly
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu
			525					530					535	Val
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln
	540						545						550	Ser
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile
	555				560						565			Asn
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His
	570				575					580				Leu
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala
585				590					595					Gln
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
	605						610						615	
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln
	620						625					630		Leu
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala

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Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn		
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Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu		
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Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile		
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Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly		
700	705	710
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala		
715	720	725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val		
730	735	740
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser		
745	750	755
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr		
765	770	775
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Leu Pro Ala Glu Lys Gln		
780	785	790
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe		
795	800	805
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu		
810	815	820
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp		
825	830	835
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly		
845	850	855
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp		
860	865	870
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu		
875	880	885
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln		
890	895	900
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly		
905	910	915
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu		
925	930	935
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly		
940	945	950
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
955	960	965

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<211> 3618

<212> DNA

<213> Unknown

<220>

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polylinker; 688-2190, esp1 mat; 2191-2226 spacer;  
2227-3615, K:trAPAO, 3616-3618, stop codon. For  
bacterial expression.

<221> CDS

<222> (1)...(3615)

<221> misc\_feature

<222> (1)...(687)  
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 1 5 10 15  
 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 atg ttg ggt ggt tgt cca aaagag cgt gca gag att tca atg ctt gaa 288  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp

145	150	155	160	
ggt ggt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta				528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	165	170	175	
ggt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac				576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc				624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	195	200	205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt				672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	210	215	220	
gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg				720
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val	225	230	235	240
gtc ggc acg act act act gtc ccc ggc acc act gcg acc gtc agc gag				768
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu	245	250	255	
ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct				816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	260	265	270	
act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt				864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly	275	280	285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc cgt gag att				912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile	290	295	300	
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag				960
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu	305	310	315	320
gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac				1008
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn	325	330	335	
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg				1056
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp	340	345	350	
aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc aat cag gat				1104
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp	355	360	365	
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct				1152
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	370	375	380	



gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp 385 390 395 400	1200
caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly 405 410 415	1248
ggg gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg 420 425 430	1296
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg 435 440 445	1344
gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc ccc aag gga Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly 450 455 460	1392
gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr 465 470 475 480	1440
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485 490 495	1488
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu 500 505 510	1536
gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act ggt Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly 515 520 525	1584
gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly 530 535 540	1632
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu 545 550 555 560	1680
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr 565 570 575	1728
ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580 585 590	1776
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595 600 605	1824
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610 615 620 625 630 635 640	1872

610	615	620	
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625 630 635 640			1920
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645 650 655			1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660 665 670			2016
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn 675 680 685			2064
gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser 690 695 700			2112
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr 705 710 715 720			2160
gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly 725 730 735			2208
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val 740 745 750			2256
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala 755 760 765			2304
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys 770 775 780			2352
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu 785 790 795 800			2400
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu 805 810 815			2448
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn 820 825 830			2496
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly 835 840 845			2544

gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 850 855 860	2592
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 865 870 875 880	2640
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr 885 890 895	2688
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tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met 945 950 955 960	2880
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tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln 1045 1050 1055	3168
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala 1060 1065 1070	3216
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe 51	3264

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Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val			
1090	1095	1100	
cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc			3360
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala			
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ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg			3408
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser			
1125	1130	1135	
aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac			3456
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn			
1140	1145	1150	
gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt			3504
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val			
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cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa			3552
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu			
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Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser			
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1205			

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Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
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Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
65				70				75						80			
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
			85					90					95				
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
		100					105					110					
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
	115					120					125						
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		

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Gly Asp His Val Thr	His Pro Asp Phe Met	Leu Tyr Asp Ala Leu Asp		
145	150	155		160
Val Val Leu Tyr Met	Asp Pro Met Cys Leu	Asp Ala Phe Pro Lys Leu		
	165	170		175
Val Cys Phe Lys Lys	Arg Ile Glu Ala Ile	Pro Gln Ile Asp Lys Tyr		
	180	185		190
Leu Lys Ser Ser Lys	Tyr Ile Ala Trp Pro	Leu Gln Gly Trp Gln Ala		
	195	200		205
Thr Phe Gly Gly Gly	Asp His Pro Pro Lys	Ser Asp Leu Val Pro Arg		
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Gly Ser Pro Glu Phe	Ala Pro Thr Val Lys	Ile Asp Ala Gly Met Val		
225	230	235		240
Val Gly Thr Thr Thr	Thr Val Pro Gly Thr	Thr Ala Thr Val Ser Glu		
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Phe Leu Gly Val Pro	Phe Ala Ala Ser Pro	Thr Arg Phe Ala Pro Pro		
	260	265		270
Thr Arg Pro Val Pro	Trp Ser Thr Pro Leu	Gln Ala Thr Ala Tyr Gly		
	275	280		285
Pro Ala Cys Pro Gln	Gln Phe Asn Tyr Pro	Glu Glu Leu Arg Glu Ile		
	290	295		300
Thr Met Ala Trp Phe	Asn Thr Pro Pro Pro	Ser Ala Gly Glu Ser Glu		
305	310	315		320
Asp Cys Leu Asn Leu	Asn Ile Tyr Val Pro	Gly Thr Glu Asn Thr Asn		
	325	330		335
Lys Ala Val Met Val	Trp Ile Tyr Gly Gly	Ala Leu Glu Tyr Gly Trp		
	340	345		350
Asn Ser Phe His Leu	Tyr Asp Gly Ala Ser	Phe Ala Ala Asn Gln Asp		
	355	360		365
Val Ile Ala Val Thr	Ile Asn Tyr Arg Thr	Asn Ile Leu Gly Phe Pro		
	370	375		380
Ala Ala Pro Gln Leu	Pro Ile Thr Gln Arg	Asn Leu Gly Phe Leu Asp		
385	390	395		400
Gln Arg Phe Ala Leu	Asp Trp Val Gln Arg	Asn Ile Ala Ala Phe Gly		
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Gly Asp Pro Arg Lys	Val Thr Ile Phe Gly	Gln Ser Ala Gly Gly Arg		
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Ser Val Asp Val Leu	Leu Thr Ser Met Pro	His Asn Pro Pro Phe Arg		
	435	440		445
Ala Ala Ile Met Glu	Ser Gly Val Ala Asn	Tyr Asn Phe Pro Lys Gly		
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Asp Leu Ser Glu Pro	Trp Asn Thr Thr Val	Gln Ala Leu Asn Cys Thr		
465	470	475		480
Thr Ser Ile Asp Ile	Leu Ser Cys Met Arg	Arg Val Asp Leu Ala Thr		
	485	490		495
Leu Met Asn Thr Ile	Glu Gln Leu Gly Leu	Gly Phe Glu Tyr Thr Leu		
	500	505		510
Asp Asn Val Thr Ala	Val Tyr Arg Ser Glu	Thr Ala Arg Thr Thr Gly		
	515	520		525
Asp Ile Ala Arg Val	Pro Val Leu Val Gly	Thr Val Ala Asn Asp Gly		
	530	535		540
Leu Leu Phe Val Leu	Gly Glu Asn Asp Thr	Gln Ala Tyr Leu Glu Glu		
545	550	555		560
Ala Ile Pro Asn Gln	Pro Asp Leu Tyr Gln	Thr Leu Leu Gly Ala Tyr		
	565	570		575
Pro Ile Gly Ser Pro	Gly Ile Gly Ser Pro	Gln Asp Gln Ile Ala Ala		
	580	585		590
Ile Glu Thr Glu Val	Arg Phe Gln Cys Pro	Ser Ala Ile Val Ala Gln		



	1060		1065		1070
Arg	Asp Thr Ser Ile Asp Val	Asp Arg Gln Trp Ser	Ile Thr Cys Phe		
	1075	1080	1085		
Met	Val Gly Asp Pro Gly Arg Lys Trp Ser	Gln Gln Ser Lys Gln Val			
	1090	1095	1100		
Arg	Gln Lys Ser Val Trp Asp Gln Leu Arg	Ala Ala Tyr Glu Asn Ala			
1105	1110	1115	1120		
Gly	Ala Gln Val Pro Glu Pro Ala Asn Val	Leu Glu Ile Glu Trp Ser			
	1125	1130	1135		
Lys	Gln Gln Tyr Phe Gln Gly Ala Pro Ser	Ala Val Tyr Gly Leu Asn			
	1140	1145	1150		
Asp	Leu Ile Thr Leu Gly Ser Ala Leu Arg	Thr Pro Phe Lys Ser Val			
	1155	1160	1165		
His	Phe Val Gly Thr Glu Thr Ser Leu Val	Trp Lys Gly Tyr Met Glu			
	1170	1175	1180		
Gly	Ala Ile Arg Ser Gly Gln Arg Gly Ala	Ala Glu Val Val Ala Ser			
1185	1190	1195	1200		
Leu	Val Pro Ala Ala				
	1205				

<210> 30

<211> 3591

<212> DNA

<213> Unknown

<220>

<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression vector pGEX-4T-1 or similar vector. gst:BEST1:sp:K:trAPAO fusion, 3591 nt.  
1-687 gst  
+ polylinker, 688-2163, BEST1 mature; 2164-2199, spacer, 2200-3588, K:trAPAO

<221> misc\_feature

<222> (1)...(687)

<223> gst + polylinker

<221> mat\_peptide

<222> (688)...(2163)

<223> BEST1 mature

<221> misc\_feature

<222> (2164)...(2199)

<223> spacer sequence

<221> misc\_feature

<222> (2200)...(3588)

<223> K:trAPAO

<221> CDS

<222> (1)...(3588)

<221> misc\_feature

<222> (2200)...(2202)

<223> Extra lysine

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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc	720
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly	



225	230	235	240	
cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc gga ata ccc Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro	245	250	255	768
tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His	260	265	270	816
gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp	275	280	285	864
tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val	290	295	300	912
agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys	305	310	315	960
ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala	325	330	335	1008
ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg	340	345	350	1056
cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac atc ctg ggc Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly	355	360	365	1104
ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser	370	375	380	1152
ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln	385	390	395	1200
agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe	405	410	415	1248
ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro	420	425	430	1296
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu	435	440	445	1344
acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg ggc gag cgc Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg	450	455	460	1392

ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu 465 470 475 480	1440
atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac ctg cgc agg Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg 485 490 495	1488
ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr 500 505 510	1536
gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu 515 520 525	1584
atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg cgc gcg ccg Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro 530 535 540	1632
atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt ggc Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly 545 550 555 560	1680
gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac ggc cgg gcc Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala 565 570 575	1728
acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat cag ttc aat Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn 580 585 590	1776
cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag ggc gcg ccc Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro 595 600 605	1824
gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga aga gcg ccg Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro 610 615 620	1872
gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu 625 630 635 640	1920
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala 645 650 655	1968
gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala 660 665 670	2016
aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser 675 680 685	2064
acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc gcg gcg gtg Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val 685 690 695	2112

690	695	700	
gtg tgc ccc gga cct tcc atc ccc cct tgc gcg gat ggc gcc aag gcg Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala 705 710 715 720			2160
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn 725 730 735			2208
gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr 740 745 750			2256
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala 755 760 765			2304
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly 770 775 780			2352
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn 785 790 795 800			2400
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu 805 810 815			2448
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr 820 825 830			2496
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala 835 840 845			2544
agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu 850 855 860			2592
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp 865 870 875 880			2640
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala 885 890 895			2688
gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu 900 905 910			2736
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala 915 920 925			2784

acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat	2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr	
930 935 940	
atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag	2880
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys	
945 950 955 960	
gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att	2928
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile	
965 970 975	
gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg	2976
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val	
980 985 990	
ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc	3024
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro	
995 1000 1005	
acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg	3072
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala	
1010 1015 1020	
gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac	3120
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp	
1025 1030 1035 1040	
aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc	3168
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser	
1045 1050 1055	
tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga	3216
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg	
1060 1065 1070	
caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg	3264
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp	
1075 1080 1085	
tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc	3312
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu	
1090 1095 1100	
cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac	3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn	
1105 1110 1115 1120	
gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg	3408
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro	
1125 1130 1135	
agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc	3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu	
1140 1145 1150	
aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta	3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu	

1155	1160	1165	
gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt			3552
Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly			
1170	1175	1180	
gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			3591
Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
1185	1190	1195	

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 <212> PRT  
 <213> Unknown

<400> 31

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		20					25					30			
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
	35					40					45				
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50				55						60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65				70					75						80
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
			85						90					95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
		100					105						110		
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
	115					120						125			
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130					135					140				
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
145					150					155					160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
			165					170						175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
		180					185						190		
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
	195					200						205			
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210				215						220				
Gly	Ser	Pro	Glu	Phe	Thr	Asp	Phe	Pro	Val	Arg	Arg	Thr	Asp	Leu	Gly
225					230					235					240
Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg	Gly	Ile	Pro
			245					250						255	
Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro	Pro	Gln	His
		260						265					270		
Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe	Gly	Ser	Asp
	275					280						285			
Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala	Pro	Gly	Val
	290					295					300				
Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser	Gly	Ala	Lys
305				310						315					320
Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly	Gly	Phe	Ala



785					790					795				800	
Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu
				805					810					815	
Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr
			820					825					830		
Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala
		835					840					845			
Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu
	850					855					860				
His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp
865					870					875					880
Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala
			885						890					895	
Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu
		900						905					910		
Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala
	915						920					925			
Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr
	930					935					940				
Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys
945					950					955					960
Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile
			965						970					975	
Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val
			980					985					990		
Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro
	995						1000					1005			
Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala
	1010					1015					1020				
Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp
1025					1030					1035					1040
Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser
			1045						1050					1055	
Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg
	1060							1065				1070			
Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp
	1075						1080					1085			
Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu
	1090					1095					1100				
Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn
1105					1110					1115					1120
Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro
			1125						1130					1135	
Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu
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Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu
	1155						1160					1165			
Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly
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Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala				
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<210> 32  
 <211> 1803  
 <212> DNA  
 <213> Unknown

<220>

<221> CDS

<222> (1)...(1803)

<223> Glyc(-)APAO coding sequence; mutation in putative  
glycosylation sites

<400> 32

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1 5 10 15	

gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
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ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
130 135 140	

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145 150 155 160	

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc	576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
180 185 190	

aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta	624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val	
195 200 205	



tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg	672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
210 215 220	
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct	720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala	
225 230 235 240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg	768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala	
245 250 255	
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa	816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln	
260 265 270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc	864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe	
275 280 285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta	912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val	
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Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile	
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agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt	1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser	
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aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa	1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	
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Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	
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Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
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Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
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Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
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Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
420 425 430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	1344

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Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile		
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tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	1440	
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile		
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acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	1488	
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser		
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gtg	gct	agc	ctg	gtg	cca	gca	gca	tag								1803	
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 <212> PRT  
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<400> 33

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Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
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Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
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			180					185					190		
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225					230					235					240
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
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Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser
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Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe
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Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile
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Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile
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Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr
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Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val
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37

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 <213> *Exophiala spinifera*

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 <212> PRT  
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Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
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Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
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Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
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Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser



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gcagcatag						1929

<210> 38

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 38

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
1				5					10					15	
Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
		35					40						45		
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85						90					95	
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120						125		
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135						140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165						170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
		180					185						190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
	195					200						205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr

210		215		220
Thr Gly Asn Ser Ile	His Gln Ala Gln Asp Gly	Thr Thr Thr Thr Ala		
225	230	235	240	
Pro Tyr Gly Asp Ser	Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
	245	250	255	
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu				
	260	265	270	
Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe				
	275	280	285	
Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val				
	290	295	300	
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile				
305	310	315	320	
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser				
	325	330	335	
Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys				
	340	345	350	
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro				
	355	360	365	
Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala				
	370	375	380	
Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys				
385	390	395	400	
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe				
	405	410	415	
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile				
	420	425	430	
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp				
	435	440	445	
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile				
	450	455	460	
Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile				
465	470	475	480	
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser				
	485	490	495	
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr				
	500	505	510	
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile				
	515	520	525	
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr				
	530	535	540	
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe				
545	550	555	560	
Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly				
	565	570	575	
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val				
	580	585	590	
Val Ala Ser Leu Val Pro Ala Ala				
	595	600		

<210> 39  
 <211> 1930  
 <212> DNA  
 <213> *Exophiala spinifera*

<220>  
 <221> intron  
 <222> (739)...(811)



<221> intron  
 <222> (1134)...(1187)

<221> misc\_feature  
 <222> (648)...(648)  
 <223> n = A,T,C or G

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 cacgtcggcg taggcccaga cggagggagg tatgtgacaa tagctggaca gattggacaa 120  
 gacgcttcgg gcgtgacaga ccctgcctac gagaaacagg ttgcccagc attcgccaat 180  
 ctgcgagctt gccttgctgc agttggagcc acttcaaacg acgtcaccaa gctcaattac 240  
 tacatcgtcg actacgcccc gagcaaactc accgcaattg gagatgggct gaaggctacc 300  
 tttgcccttg acaggctccc tccttgcaag ctggtgcccag tgcgggcctt gtcttcacct 360  
 gaatacctct ttgaggttga tgccacggcg ctggtgcccg gacacacgac cccagacaac 420  
 gttgcggacg tggtagtggt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480  
 caggccgccc gtctgtcctg cctcgcttctt gaggcgatgg atcgtgtagg gggaaagact 540  
 ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600  
 aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt ggagggcgag 660  
 ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720  
 ccttatgggt actccttggt aagcacaate ccactttgtg atgagacctc tgcgagtggt 780  
 agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840  
 ggaactcctc cccgtatggt ctcagctgat cgaagagcat agccttcaag acctcaaggc 900  
 gagccctcag gcgaagcggc tcgacagtgt gagcttcgag cactactgtg agaaggaact 960  
 aaacttgctt gctgttctcg gcgtagcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020  
 agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcc aagggtctcag 1080  
 taatattttc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa cagggtgcgtg 1140  
 tgggtgctgc tcaggtgggg gactcgtttc tcaagtgggtc atttcaggta tgcagtcgat 1200  
 ttgccatgcc atgtcaaagg aacttggttc aggtcagtg cacctcaaca ccccgctcgc 1260  
 tgaaattgag cagtcggcat ccggctgtac agtacgatcg gcctcggggc ccgtgttccg 1320  
 aagcaaaaag gtggtggttt cgttaccgac aaccttgat cccacctga cattttcacc 1380  
 acctctcccc gccgagaagc aagcattggc ggaaaattct atcctgggct actatagcaa 1440  
 gatagtcttc gtatgggaca agcgtggtg gcgcgaacaa ggcttctcgg gcgtcctcca 1500  
 atcgagctgt gaccccatct catttgccag agataccagc atcgacgtcg atcgacaatg 1560  
 gtccattacc tgtttcatgg tcggagaccc gggacggaag tgggtcccaac agtccaagca 1620  
 ggtacgacaa aagtctgtct gggaccaact ccgcgcagcc tacgagaacg ccggggccca 1680  
 agtcccagag ccggccaacg tgctcgaaat cgagtgggtc aagcagcagt atttccaagg 1740  
 agctccgagc gccgtctatg ggctgaacga tctcatcaca ctgggttcgg cgctcagaac 1800  
 gccgttcaag agtgttcatt tcgttgggaa ggagacgtct ttagtttgga aagggtatat 1860  
 ggaagggggc atacgatcgg gtcaacgagg tgctgcagaa gttgtggcta gcctggtgcc 1920  
 agcagcatag 1930

<210> 40  
 <211> 598  
 <212> PRT  
 <213> Exophiala spinifera

<220>  
 <221> VARIANT  
 <222> (216)...(216)  
 <223> Xaa = Any Amino Acid

<400> 40  
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  
 1 5 10 15  
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
 20 25 30



Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn
			500					505					510		
Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp
		515					520					525			
Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu
	530					535					540				
Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser
545				550						555					560
Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met
			565					570					575		
Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala
		580					585					590			
Ser	Leu	Val	Pro	Ala	Ala										
		595													

<210> 41  
 <211> 1928  
 <212> DNA  
 <213> *Rhinocycladiella atrovirens*

<220>  
 <221> intron  
 <222> (739)...(811)

<221> intron  
 <222> (1134)...(1185)

<400> 41

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cacgtcggcg	taggcccaca	cggagggagg	tatgcgacaa	tagctggaca	gattggacaa	120
gacgcttcgg	ccgtgacaga	ccctgcctac	gagaaacagg	ttgcccagc	attcgccaac	180
ctgcgagctt	gtcttgctgc	agttggagcc	acttcaaacg	acattaccaa	gctcaattac	240
tacatcgctg	actacaaccc	gagcaaactc	accgcaattg	gagatgggct	gaaggctacc	300
tttgcccttg	acaggctccc	tccttgacag	ctgggtgccg	tgccggccct	ggcttcacct	360
gaatacccct	ttgaggttga	tgccacggcg	ctgggtccag	gacactcaac	cccagacaat	420
gttgcggacg	tggtcgtggt	gggcgctggc	ttgagcgggt	tggagacggc	acgcaaagtc	480
caggctgccc	ggctgtcctg	cctcgcttct	gaggcgatgg	atcgtgtggg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggacg	gctatcaatg	acctcggcgc	tgctgtggatc	600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatgggt	attccctggg	aagcacaatt	ccatcttggt	atgagacctc	tgctgtgtgt	780
agaatacagt	cgctgactcc	acatcgctcc	gctgagcgag	gaggttgcaa	gtgcactcgc	840
ggaactcctt	cccgcattgg	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aagcttgccct	gctgttctcg	gcgtggcaca	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcga	ccggtctcag	1080
taatattgtc	tcggataaga	aagacgggtg	gcagtatatg	cgatgcaaaa	cagggtgcgtg	1140
tggtgttctc	tcagtgggag	actcgtttct	tagtgggtcat	tcagggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttggtccag	gctcagtgcg	cctcaacacc	cccgtcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcgggcggc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttggtatcc	caccttgata	ttttcaccac	1380
ctcttcccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttctg	atgggacaag	ccgtgggtgg	gcgaacaagg	cttctcgggc	gtcctccaat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
ccattacctg	tttcatgggc	ggagaccggg	gacggaagtg	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtcttg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccacg	1680
tcccagagcc	ggccaacgtg	ctcgagatcg	agtggctcga	gcagcagtat	ttccaaggag	1740
cgccgagcgt	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800

cggtcaaggg tgttcatttc gttggaacgg agacgtcttt gggtttggaaa gggatatatgg 1860  
aagggggccat acgatcggggt cagcgaggcg ctgcagaagt tgtggctagc ctgggtgccag 1920  
cagcatag 1928

<210> 42  
<211> 598  
<212> PRT  
<213> Rhinocycladiella atrovirens

<400> 42  
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro  
1 5 10 15  
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Ala  
20 25 30  
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro  
35 40 45  
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
50 55 60  
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr  
65 70 75 80  
Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
85 90 95  
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
100 105 110  
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala  
115 120 125  
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val  
130 135 140  
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
145 150 155 160  
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
165 170 175  
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile  
180 185 190  
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
195 200 205  
Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly  
210 215 220  
Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr  
225 230 235 240  
Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu  
245 250 255  
Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro  
260 265 270  
Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His  
275 280 285  
Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn  
290 295 300  
Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met  
305 310 315 320  
Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile  
325 330 335  
Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly  
340 345 350  
Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser  
355 360 365  
Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly  
370 375 380

Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Gly	Val	Phe	Arg	Ser	Lys	Lys	Val
385					390					395					400
Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Ile	Phe	Ser	Pro
				405					410					415	
Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Lys	Ser	Ile	Leu	Gly
			420					425					430		
Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu
		435					440					445			
Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe
	450					455				460					
Ala	Arg	Asp	Thr	Ser	Ile	Glu	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys
465					470				475						480
Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln
				485					490					495	
Val	Arg	Gln	Lys	Ser	Val	Trp	Asn	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn
			500					505					510		
Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp
		515					520					525			
Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Val	Val	Tyr	Gly	Leu
	530					535					540				
Asn	Cys	Leu	Asn	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Gly
545					550					555					560
Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met
				565					570					575	
Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala
			580					585					590		
Ser	Leu	Val	Pro	Ala	Ala										
		595													

<210> 43  
 <211> 1928  
 <212> DNA  
 <213> Rhinocycladiella atrovirens

<220>  
 <221> intron  
 <222> (739)...(811)

<221> intron  
 <222> (1134)...(1186)

<400> 43	
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gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaac	180
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac	240
tacatcgtcg actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc	300
tttgcccttg acaggctccc tccttgcaag ctgggtgccg tgccggccct ggcttcacct	360
gaatacctct ttgaggttga tgccacggcg ctgggtccag gacactcaac cccagacaat	420
gttgcggacg tggctcgtggt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc	480
caggctgccg ggctgtcctg cctcgttctt gaggcgatgg atcgtgtggg gggaaagact	540
ctgagcgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgcgtggatc	600
aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct	720
ccttatggtg attccctggt aagcacaatt ccatcttggt atgagacctc tgcgtgtgt	780
agaatacagt cgctgactcc acatcgtcca gctgagcgag gaggttgcaa gtgcactcgc	840
ggaactcctt cccgcatggt ctcagctgat cgaagagcat agtcttgaag accccaaggc	900
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct	960

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aaacttgccct gctgtttctcg gcggtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020
agcccacgag atcagcatgt tttttctcac cgactacatc aagagtgcca ccggtctcag 1080
taatattgtc tcggataaga aagacgggtgg gcagtatatg cgatgcaaaa caggtgcgtg 1140
tggtgtttctc tcagtgggag actcgtttct tagtggatcat tccaggtatg cagtcgcttt 1200
gccatgccat gtcaaaggaa cttgtttccag gctcagtga cctcaacacc cccgtcgccg 1260
aaattgagca gtcggcatcc ggctgtacag tacgatcggc ctcgggaggc gtgttccgaa 1320
gtaaaaaggt ggtggtttcg ttaccgacaa ccttgatcc cacttgata ttttcaccac 1380
ctcttcccgc cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga 1440
tagtcttctg atgggacaag ccgtgggtgg gcgaacaagg cttctcgggc gtcttccaat 1500
cgagctgtga ccccatctca ttgcccagag ataccagcat cgaagtcgat cggcaatggt 1560
ccattacctg tttcatggtc ggagaccggg gacggaagtg gtcccaacag tccaagcagg 1620
tacgacagaa gtctgtctgg aaccaactcc gcgcagccta cgagaacgcc ggggcccaag 1680
tcccagagcc ggccaacgtg ctcgagatcg agtggtcgaa gcagcagtat ttccaaggag 1740
cgccgagcgc cgtctatggg ctgaactgtc tcaacacact ggggttcggcg ctcagaacgc 1800
cgttcaaggg tgttcatttc gttggaacgg agacgtcttt ggtttggaaa gggatatatg 1860
aaggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtggctagc ctggtgccag 1920
cagcatag 1928

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<210> 44

<211> 591

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 44

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
1          5          10          15
Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val
20          25          30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35          40          45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50          55          60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65          70          75          80
Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85          90          95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100         105         110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115         120         125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130         135         140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145         150         155         160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165         170         175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
180         185         190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
195         200         205
Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210         215         220
Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
225         230         235         240
Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
245         250         255
Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
260         265         270

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Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
 275 280 285  
 Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg  
 290 295 300  
 Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr  
 305 310 315 320  
 Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys  
 325 330 335  
 Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu  
 340 345 350  
 Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn  
 355 360 365  
 Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg  
 370 375 380  
 Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr  
 385 390 395 400  
 Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
 405 410 415  
 Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
 420 425 430  
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
 435 440 445  
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu  
 450 455 460  
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
 465 470 475 480  
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
 485 490 495  
 Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 500 505 510  
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 515 520 525  
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly  
 530 535 540  
 Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu  
 545 550 555 560  
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 565 570 575  
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 580 585 590

<210> 45  
 <211> 1928  
 <212> DNA  
 <213> *Rhinocycladiella atrovirens*

<220>  
 <221> intron  
 <222> (739)...(811)

<221> intron  
 <222> (1134)...(1185)

<400> 45  
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 gacgcttcgg ccgtgacaga cctgcctac gagaaacagg ttgcccaagc attcgccaac 180  
 ctgcgagctt gtcttgctgc agttggagcc acttcaaagc acattaccaa gctcaattac 240

tacatcgctcg	actacaaccc	gagcaaactc	accgcaattg	gagatgggct	gaaggctacc	300
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccag	tgccggccct	ggcttcacct	360
gaataacctct	ttgaggttga	tgctacggcg	ctgggtccag	gacactcaac	cccagacaat	420
gttgcgagcg	tggtcgtggt	gggcgctggc	ttgagcggtt	tgagacggc	acgcaaagtc	480
caggctgccg	ggctgtcctg	cctcgttctt	gaggcgatgg	atcgtgtggg	gggaaagact	540
ctgagcgtag	aatcgggtcc	cggcaggacg	actatcaatg	acctcggcgc	tgctgtggatc	600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
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agaatacagt	cgctgactcc	acatcgctca	gctgagcgag	gaggttgcaa	gtgcaactcg	840
ggaactcctt	cccgcattgt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
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taatattgtc	tcggataaga	aagacggtgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
tggtgttctc	tcagtgggag	actcgtttct	tagtgggtcat	tccaggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttggtccag	gctcagtgc	cctcaacacc	cccgtcgccg	1260
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gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttgatcc	caccttgata	ttttcaccac	1380
ctcttcccg	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
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cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
ccattacctg	tttcatggtc	ggagaccggc	gacggaagtg	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccaag	1680
tcccagagcc	ggccaacgtg	ctcgagatcg	agtgggtcgaa	gcagcagtat	ttccaaggag	1740
cgccgagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tgttcatttc	gttggaaacg	agacgtcttt	ggtttggaag	gggtatatgg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtgcctagc	ctggtgccag	1920
cagcatag						1928

<210> 46

<211> 591

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 46

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Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val	Thr
			20					25					30		
Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro	Ala
		35					40					45			
Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	Leu
	50					55					60				
Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr	Tyr
65					70					75				80	
Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	Leu
			85					90						95	
Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	Pro
			100					105					110		
Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	Thr
		115					120					125			
Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	Val
		130					135					140			
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
145					150					155				160	
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
			165					170						175	



Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
			180					185					190		
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Phe
		195					200				205				
Lys	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
	210					215					220				
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro
225					230					235					240
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
			245					250						255	
Leu	Leu	Pro	Ala	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Glu	Asp
			260					265					270		
Pro	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Gln	Leu	Asp	Ser	Val	Ser	Phe	Ala
	275						280					285			
His	Tyr	Cys	Glu	Lys	Asp	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala
	290					295					300				
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser
305					310					315					320
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn
			325						330					335	
Ile	Val	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr
			340				345						350		
Gly	Met	Gln	Ser	Leu	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly
	355					360						365			
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser
	370					375					380				
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Gly	Val	Phe	Arg	Ser	Lys	Lys
385					390					395					400
Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Ile	Phe	Ser	Pro	Leu
			405						410					415	
Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Lys	Ser	Ile	Gly	Tyr	Tyr	Ser
			420					425					430		
Lys	Ile	Val	Phe	Val	Asp	Lys	Leu	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser
	435					440						445			
Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr
	450					455					460				
Ser	Ile	Glu	Val	Asp	Arg	Gln	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp
465					470					475					480
Pro	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val
			485						490					495	
Trp	Asn	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro
			500					505					510		
Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe
	515						520					525			
Gln	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Cys	Leu	Asn	Thr	Leu	Gly
	530					535					540				
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Gly	Val	His	Phe	Val	Gly	Thr	Glu
545					550					555					560
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
			565						570					575	
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Pro	Ser	Leu	Val	Pro	Ala	Ala	
			580					585					590		

<210> 47  
 <211> 600  
 <212> PRT  
 <213> Exophiala spinifera

<400> 47

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75					80
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85						90					95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120						125		
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135						140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155					160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165						170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
			180					185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
		195				200						205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
	210					215					220				
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225				230						235					240
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
			245						250					255	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln
		260					265						270		
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
	275					280						285			
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val
	290				295						300				
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
305				310						315					320
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser
			325						330					335	
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys
		340						345					350		
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro
	355					360						365			
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala
	370				375						380				
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys
385				390						395					400
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe
			405						410					415	
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile
		420						425					430		
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp
	435					440						445			
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile

450		455		460
Ser Phe Ala Arg Asp Thr	Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
465	470	475		480
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser				
	485	490		495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr				
	500	505		510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile				
	515	520		525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr				
	530	535		540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe				
545	550	555		560
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly				
	565	570		575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val				
	580	585		590
Val Ala Ser Leu Val Pro Ala Ala				
	595	600		

<210> 48

<211> 1392

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteine 461

<400> 48

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
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ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	

100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125			384
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140			432
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160			480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175			528
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190			576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205			624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 210 215 220			672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240			720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255			768
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270			816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285			864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300			912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320			960
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335			1008

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	
450 455 460	

<210> 49  
 <211> 463  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Cys (-) APAO; removal of cysteine 461

<400> 49																	
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly		
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val		
			20				25						30				
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser		
		35					40					45					
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn		
	50				55					60							
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu		
65					70				75					80			
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln		
			85					90					95				
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu			
		100					105					110					
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Pro	Val	Trp	Ser	Gln	Leu			
		115					120										

Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
130						135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
				165					170					175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	210					215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
	275						280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
				325					330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
		340						345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
	355						360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390					395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
			405						410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
		420						425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
	435					440						445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
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<210> 50

<211> 1392

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 50

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Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
1				5					10				15		

48

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggg ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	
450 455 460	

<210> 51  
<211> 463



<212> PRT  
 <213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
			20				25						30		
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
		35					40					45			
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
	50				55					60					
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65					70					75					80
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
			85					90						95	
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
			100				105						110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
	130					135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
			165					170						175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180				185						190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
	195					200						205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala
	210					215				220					
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
			245					250						255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260					265						270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
		275					280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325					330						335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
		340					345					350			
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
	355					360						365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385				390						395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly

				405					410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
			420					425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
		435					440					445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
		450				455					460				

<400> 52																	
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Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly		
1				5					10					15			
ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggt	ctg	agc	tcc	ctc	gtt	96	
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Ser	Leu	Val		
			20					25					30				
ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg	144	
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser		
		35					40					45					
ggt	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	192	
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn		
	50					55					60						
gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	240	
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu		
65					70					75					80		
gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	288	
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln		
			85						90					95			
gac	ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	336	
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu		
			100					105					110				
gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	384	
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu		
		115					120					125					
atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	432	
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys		
	130					135					140						
cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	480	

Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn		
145					150					155					160		
ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	528	
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu		
				165					170					175			
ggc	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	576	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile		
			180					185					190				
aag	agt	gcc	acc	ggc	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	624	
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly		
		195					200					205					
ggg	cag	tat	atg	cga	tgc	aaa	aca	ggc	atg	cag	tcg	att	tcg	cat	gcc	672	
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala		
	210					215				220							
atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	720	
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val		
225					230					235					240		
gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	768	
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser		
				245					250					255			
ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	816	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr		
			260					265					270				
ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	864	
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln		
		275					280					285					
gca	ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	912	
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe		
	290					295					300						
gta	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	960	
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu		
305					310					315					320		
caa	tcg	agc	tcc	gac	ccc	atc	tca	ttt	ggc	aga	gat	acc	agc	atc	gac	1008	
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp		
				325					330					335			
gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	1056	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly		
			340					345					350				
cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	1104	
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp		
		355					360					365					
gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	1152	
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu		
	370					375					380						

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa 1200  
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 385 390 395 400

tgc	gcg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	1296
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	
			420					425					430			

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392  
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala \*  
450 455 460

<220>  
<223> Cys (-) APAO; removal of cysteines 169, 359, and 461

	<400> 53														
Lys 1	Asp	Asn	Val	Ala 5	Asp	Val	Val	Val	Val	Gly 10	Ala	Gly	Leu	Ser	Gly 15
Leu	Glu	Thr	Ala 20	Arg	Lys	Val	Gln	Ala 25	Ala	Gly	Leu	Ser	Ser	Leu	Val 30
Leu	Glu	Ala 35	Met	Asp	Arg	Val	Gly 40	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser 45
Gly 50	Pro	Gly	Arg	Thr	Thr	Ile 55	Asn	Asp	Leu	Gly	Ala 60	Ala	Trp	Ile	Asn 65
Asp 65	Ser	Asn	Gln	Ser	Glu 70	Val	Ser	Arg	Leu	Phe 75	Glu	Arg	Phe	His	Leu 80
Glu	Gly	Glu	Leu	Gln 85	Arg	Thr	Thr	Gly	Asn 90	Ser	Ile	His	Gln	Ala 95	Gln 100
Asp	Gly	Thr	Thr 100	Thr	Thr	Ala	Pro	Tyr 105	Gly	Asp	Ser	Leu	Leu	Ser	Glu 110
Glu	Val	Ala 115	Ser	Ala	Leu	Ala	Glu 120	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu 125
Ile 130	Glu	Glu	His	Ser	Leu	Gln 135	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys 140
Arg 145	Leu	Asp	Ser	Val	Ser 150	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn 160
Leu	Pro	Ala	Val	Leu 165	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu 175
Gly	Val	Glu	Ala 180	His	Glu	Ile	Ser	Met 185	Leu	Phe	Leu	Thr	Asp	Tyr	Ile 190
Lys	Ser	Ala 195	Thr	Gly	Leu	Ser	Asn 200	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly 205

Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala
210						215				220					
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
			260					265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
		275					280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
				325					330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
			340					345					350		
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Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
				405					410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
			420					425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
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